PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of

MARCIREAU ET AL

Serial No.: **09/744,125**

Filed: September 17, 2001

Title: MEKKI-INTERACTING FHA PROTEIN

Examiner: Slobodyansky, E.

Art Unit: 1652

hereby certify that this correspondence is being transmitted via facsimile to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, care of Art Unit 1646 at 703-305-3014 on

Date of Deposit

Printed Name of Person Signing Certificate

Signature

DECLARATION UNDER 37 CFR § 1.131 OF PRIOR INVENTION IN A WORLD TRADE ORGANIZATION (WTO) MEMBER COUNTRY

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313

Dear Sir:

Christophe Marcireau declares as follows:

1.   I am an inventor of the inventions claimed in U.S. Patent Application Serial No. 09/744,125 filed on September 17, 2001 ("the '125 application").

2.   Prior to September 10, 1997 I obtained the nucleic acid of SEQ ID NO:1 in France, a WTO member country.

3.   Prior to September 10, 1997, I translated SEQ ID NO:1 and obtained the amino acid sequence of SEQ ID NO:2 in France, a WTO member country.

4.   Attached hereto is a machine-generated graph that shows the results of the sequencing of the nucleic acid of SEQ ID NO:1. The sequencing of SEQ ID

NO:1 and its translation to obtain the amino acid sequence of SEQ ID NO:2 was performed under my direction. The machine-generated date on the graph has been redacted, but that date is prior to September 10, 1997. The sequencing was conducted in France, a WTO member country.

5.   I declare that all of the foregoing statements are true, recognizing that willful false statements are punishable by fine or imprisonment, or both, under 18 U.S.C. § 1001, and that any such willful false statements may jeopardize the validity of the application or any patent that issues from it.

Date: _October the 12th_   _____
                              Christophe Marcireau

DNA sequence 1603 b.p. GTGGATCCCCCG ... TCGCCCTATAGT linear

4909+8855+8955+8856+6196 mekk1bp3

```
1/1                                    31/11
GTG GAT CCC CCG GGC TGC AGG AAT TCG GCA CGA GGT GGG GTG GAA CCA GGG CGC TGT TCG
 V   D   P   P   G   C   R   N   S   A   R   G   G   V   E   P   G   R   C   S
61/21                                  91/31
GGG AGT GAA CCC TCC TCC AGT GAG AAA AAG AAG GTA TCC AAA GCC CCC AGC ACT CCT GTG
 G   S   E   P   S   S   S   E   K   K   K   V   S   K   A   P   S   T   P   V
121/41                                 151/51
CCA CCC AGC CCA GCC CCA GCC CCT GGA CTC ACC AAG CGT GTG AAg AAg AGT AAA CAG CCA
 P   P   S   P   A   P   A   P   G   L   T   K   R   V   K   K   S   K   Q   P
181/61                                 211/71
CTT CAG GTG ACC AAG GAT CTG GGC CGC TGG AAg CCT GCA AAT GAC CTC CTG CTC ATA AAT
 L   Q   V   T   K   D   L   G   R   W   K   P   A   N   D   L   L   L   I   N
241/81                                 271/91
GCT GTG TTG CAg ACC AAC GAC CTG ACC TCC GTC CAC CTG GGC GTG AAA TTC AGC TGC CGC
 A   V   L   Q   T   N   D   L   T   S   V   H   L   G   V   K   F   S   C   R
301/101                                331/111
TTC ACC CTT CGG GAG GTC CAG GAG CGT TGG TAC GCC CTG CTC TAC gAT CCT GTC ATC TCC
 F   T   L   R   E   V   Q   E   R   W   Y   A   L   L   Y   D   P   V   I   S
361/121                                391/131
AAG TTG GCC TGT CAG GCC ATG AGG CAG CTG CAC CCA GAG GCT ATT GCA GCC ATC CAG AGC
 K   L   A   C   Q   A   M   R   Q   L   H   P   E   A   I   A   A   I   Q   S
421/141                                451/151
AAG GCC CTG TTT AGC AAG GCT GAG GAG CAG CTG CTG AGC AAA GTG GGA TCG ACC AGC CAG
 K   A   L   F   S   K   A   E   E   Q   L   L   S   K   V   G   S   T   S   Q
481/161                                511/171
CCC ACC TTG GAG ACC TTC CAG GAC CTG CTG CAC AGA CAC CCT GAT GCC TTC TAC CTG GCC
 P   T   L   E   T   F   Q   D   L   L   H   R   H   P   D   A   F   Y   L   A
541/181                                571/191
CGT ACC GCG AAG GCC CTG CAG GCC CAC TGG CAG CTC ATG AAG CAG TAT TAC CTG CTG GAG
 R   T   A   K   A   L   Q   A   H   W   Q   L   M   K   Q   Y   Y   L   L   E
601/201                                631/211
GAC CAG ACA GTG CAG CCG CTG CCC AAA GGG GAC CAA GTG CTG AAC TTC TCT GAT GCA GAG
 D   Q   T   V   Q   P   L   P   K   G   D   Q   V   L   N   F   S   D   A   E
661/221                                691/231
GAC CTG ATT GAT GAC AGT AAG CTC AAG GAC ATG CGA GAT GAG GTC CTG GAA CAT GAG CTG
 D   L   I   D   D   S   K   L   K   D   M   R   D   E   V   L   E   H   E   L
721/241                                751/251
ATG GTG GCT GAC CGG CGC CAG AAG CGA GAG ATT CGG CAG CTG GAA CAG GAA CTG CAT AAG
 M   V   A   D   R   R   Q   K   R   E   I   R   Q   L   E   Q   E   L   H   K
781/261                                811/271
TGG CAG GTG CTA GTG GAC AGC ATC ACA GGC ATG AGC TCT CCG GAC TTC GAC AAC CAg ACA
 W   Q   V   L   V   D   S   I   T   G   M   S   S   P   D   F   D   N   Q   T
841/281                                871/291
CTG GCA GTG CTG CGG GGC CGC ATG GTG CGG TAC CTG ATG CGC TCG CGT GAG ATC ACC CTG
 L   A   V   L   R   G   R   M   V   R   Y   L   M   R   S   R   E   I   T   L
901/301                                931/311
GGC AGA GCA ACC AAG GAT AAC CAG ATT GAT GTG GAC CTG TCT CTG GAG GGT CCG GCC TGG
 G   R   A   T   K   D   N   Q   I   D   V   D   L   S   L   E   G   P   A   W
961/321                                991/331
AAG ATA TCC CGG AAA CAA GGT GTC ATC AAG CTG AAG AAC AAC GGT GAT TTC TTC ATT GCC
 K   I   S   R   K   Q   G   V   I   K   L   K   N   N   G   D   F   F   I   A
1021/341                               1051/351
AAT GAG GGT CGA CGG CCC ATC TAC ATC GAT GGA CGG CCG GTG CTC TGT GGC TCC AAA TGG
 N   E   G   R   R   P   I   Y   I   D   G   R   P   V   L   C   G   S   K   W
1081/361                               1111/371
CGC CTC AGC AAC AAC TCT GTG GTG GAG ATC GCC AGC CTG CGA TTC GTC TTC CTT ATC AAC
 R   L   S   N   N   S   V   V   E   I   A   S   L   R   F   V   F   L   I   N
1141/381                               1171/391
CAG GAC CTC ATT GCC CTC ATC AGG GCT GAG CTG CCA AGA TCA CAC CAC AGT GAG GAA TGG
 Q   D   L   I   A   L   I   R   A   E   L   P   R   S   H   H   S   E   E   W
1201/401                               1231/411
TGG CAG GAC TCG TGG GCC CTC TCC GGC CTG TTT CCC CTG CCA CTC CAG CCC CCT TGA
 W   Q   D   S   W   A   L   S   G   L   F   P   L   P   L   Q   P   P   *
```
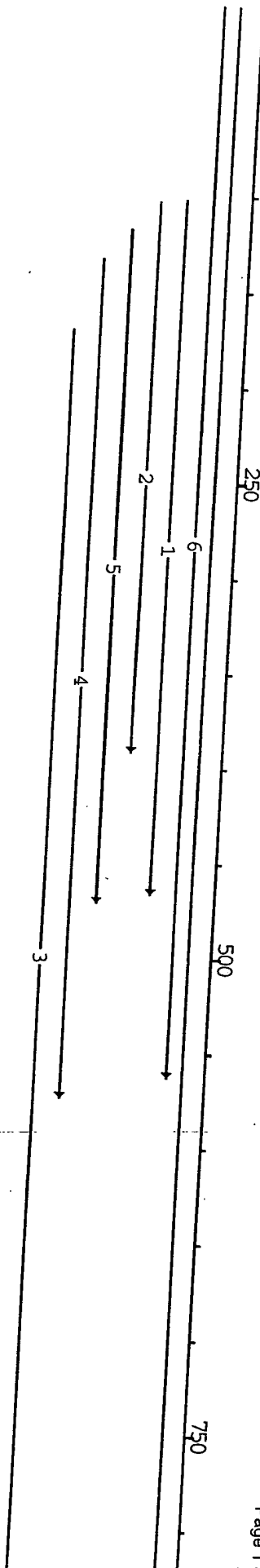
AutoAssembler™ 1.4.0

Ass EST

250

500

750

6

1

2

5

4

3

Project: Ass EST
Last saved: ▬▬▬▬▬▬▬▬▬▬▬   16:09:01
Last assembled: ▬▬▬▬▬▬▬▬▬▬▬   16:09:55

Threshold: 10.0 Error Rate: 5.0%
Window: 13 Offset: 0 Tolerance: 1 Hit Count: 10 Overlap: 10%

	Sequences	Bases	Percent
Total in project:	6	2576	100.0%
Total in assemblages:	6	2576	100.0%
Total unassembled:	0	0	0.0%
Total dye primer:	0	0	0.0%
Total dye terminator:	0	0	0.0%
Non-373 sequences:	6	2666	103.5%

	Sequences	Bases	Score	Ambiguities
w26888.Assemblage.1	6	831	1773.0	34

---

w26888.Assemblage.1	Sequences:	6	Bases:	831	Score:	1773.0
Redundancy	Average:	3.2	High:	6	Low:	1
Sequence Lengths	Average:	429	High:	640	Low:	282

File	Sample		ID	Begin	End	Length	Date	Chemistry
w26888		->	6	0	562	535	12/03/97	
aa134651		->	1	103	467	352	12/03/97	
f12127		->	2	104	392	282	12/03/97	
w00383		->	5	119	472	347	12/03/97	
t66207		->	4	135	575	420	12/03/97	
r52839		->	3	172	831	640	12/03/97	

Unassembled Sequences	Sequences:	0 Bases:	0		
File	Sample	ID	Begin	End	Length	Date	Chemistry

SIMPS 4S

Applied Biosystems

untitled 2

AutoAssembler™ 1.4.0

v26888.Assemblage.1 GGnnnnTACCCAGACGACGGACCCTCCAGAGACAGGTCCACATCAATCTGGTTATCCTTGGTTGCTCTGCCCAGGTGATCTCACGCGGCAGCCATCAGTTACGCGGCAGCCATCAGTTACGCGGCAGCCATCAGTTCCGCGAAGCCggCTTT-G

v26888 ->   GGNNNNTACCCAGACGACGGACCCTCCAGAGACAGGTCC   CCGCGAAGCCggCTTT-G
aa134651 -> ACGGAAGCCCGGCTTT-G
12127 -> CGGAAGCGNNCTTTTG
v00383 -> G

v26888.Assemblage.1 GCCCTGCGGCTGCTACCGTCGCCGCGGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGTT

v26888 -> GCCCTGCGGGCTGCTACCGTCGCCGCGGGGAGAAATTGTTGGATCTGGCAGTCTAGGNAGTCTAGGAATGAATCTCCTCCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGGNT
aa134651 -> GCC--TGCGGCTGCTACCGTCGCCGCGGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGTT
12127 -> GCCCTGCGGCGTGCTACCGTCGCNGCGGNGGAGAAATTGTTGGNTCTGGCAGTCTAGGAATGANTCTCCTCCAGCNTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGTT
v00383 -> GCC-TGCGGCTGCTACCGTCGCCGCGGGGAGAAATTGTTGGANCTGGCAGTCTAGGAATGAATCTCCTCCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGTT
66207 -> CCGTCGCGC--CGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGTT
52839 -> CCGTCGCGC--CGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGGATGAGCCTGTGGGACCGTT

v26888.Assemblage.1 CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAAAGATTCTCAGGGCACT-GCCAGCCG-CTCA-GAG

v26888 -> CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGNATCAGGCACT-GCCAGNCG-CTCAAGAG
aa134651 -> CCTCCTAGCCCGTGGTTTGGAACCAGTGGCTTTGGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAAAGATTCTCAGGGCACT-GCCAGCCGNGCTCA-GAG
12127 -> CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGGACTGTNAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAAAGATTCATCCCTGATGGCATCAAAGATTCTCAGGGCACT-GCCAGCCG-CTCA-GAG
v00383 -> CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAAAGATTCTCAGGGCACT-GC-AGCCG--AGCCG-CTCA-GAG
66207 -> CCTCCTAGCCCGTGGTTTGGAACCAGTGGCTTTGGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAAAGATTCTCAGGGCACT-GC--AGCCG-CTCA-GAG
52839 -> CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAAAGATTCTCAGGGCACT-GCCAGCCG-CTCA-GAG

v26888.Assemblage.1 GATGAGGAGTCACTGGCAGGGCAGAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGG-a-CCATCCC-TAAAC-GGAGAA-GCTCCTCCAAGgT-CATCAAGAGGAAGAAGTTC-GaTGAT

v26888 -> GATGAGGAGTCACTGGCAGGGNA-GAA-GC-GA-GCCTCCTCCCA-GGCCTTGGG-NACCATCCCTAAAC-GGAGAA-GNTCCTCCCAGGT-CANCAAGACGA-GAAGT-CCGNTGAT
aa134651 -> GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GCCGA-GCCTCC-TCCCAAGGCCTTGGG-CACCATCCC-TAAAC-GGAGAA-GCTCCTCCCAAGGTTCATCAAGAGGAAGAAGTTC-GaTGAT
12127 -> GATGAGGAGTCACTGGCAGGGCA-GAA-GN-G
v00383 -> GATGAGGAGTCACTGGCAGGGCAAGAAAGC-GAAGCCTCC-TCCCAAGACCCTAAAC-TCCCAAGGTTCATCAAGAGGAAGAAGAAGTTC-GaTGAT
66207 -> GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGG-A-CCATCCC-TAAAC-GGAGAA-GCTCCTCCCAGGTT-TATCAAGAGGAAGAAGTTC-GaTGAT
52839 -> GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGGCA-CCATCCC-TAAAC-GGAGAA-GCTCCTCCCAGGTT-CATCAAGAGGAAGAAGTTC-GaTGAT

untitled 2

Applied Biosystems

AutoAssembler™ 1.4.0

```
                              500        525        550        575        600
v26888.Assemblage.1 GAGcTgGtGGAGAGacAGCCTGGmAAaTcTtCTtaCCCggCggcAAAGGGgGCcAgt-GGG-tkGAaCCAGGGgcgcTkcT-CGGGGAGTGAACCcTCCTCCAGTGAGAAGAAGAAGGTATT
                                      .    .      .  .       .   .   .
v26888           -> GAATTNGNGGAGAAAAGCCTGGAAA--TNT-CTT-CCCCGN-AAAGGGG-CAAN--GGG-NTGACCCAGGGG---TTNT-CG

t66207           -> GAGCTGGTGGAGAGCAGCCTGGNAAAAATCTTCTTACCCGGGCAAAGGGGGCGCTNTTTCGGGGAGTGAACC--T
c52839           -> GAGCTGGTGGAGAGCAGCCTGGCAAAAATCTTCT-ACCCGGCAAAGGGGGCCAGT-GGGTGGAACCAGGG-CGCTGTT-CGGGGAGTGAACCCTCCTCCAGTGAGAAGAAGAAGGTATT

                              625        650        675        700
v26888.Assemblage.1 CCAAAGCCCCCAGCACTCCTGTGCCCACCCAGCCCCCTGGGATTCACCCAGCCCCAGCGTGTGAAGAGAGTAAACAGCCATTTTCAGGTGAACCAAGGATCTTGGGCCGTTGGAA

:52839           -> CCAAAGCCCCCAGCACTCCTGTGCCCACCCAGCCCCCTGGGATTCACCCAGCCCCAGCGTGTGAAGAAGAGTAAACAGCCATTTTCAGGTGAACCAAGGATCTTGGGCCGTTGGAA

                              725        750        775        800        825
v26888.Assemblage.1 GCTTGCAGATTGAnCTTCTTmTTTATTAAATTGTTGTGTTTGCAGACCAACGACTTAACTTCnTTCACTTGGGnTGAAATTTnAGTTNCCGTTTAACCTTTnGGAAGTTCAG

:52839           -> GCTTGCAGATTGAnCTTCTTNTTTATTAAATTGTTGTGTTTGCAGACCAACGACTTAACTTCnTTCACTTGGGnTGAAATTTnAGTTNCCGTTTAACCTTTnGGAAGTTCAG
```

debut m mine

ABI PRISM™

Model 377
Version 2.1.1

22•CM 5

CM 5
Lane 22

Signal G:406 A:809 T:268 C:303
*DT4%Ac{A Set-AnyPrimer)
S/N 95080645
Points 1207 to 11812   Base 1: 1207

Spacing: 11.23 ABI100

GGGGGGGGGG TATNTA ACCCAA AAAAANA CNCCTAG AA T AGT GG ATCCCCC GGGGCT GCAGG AATTCG GCACG AGG TGGGG TGG AACCAGG CG CTG T TCGGGG AGTG AACCCT CTCCGAGTG AG AAAAG AAGG T ATCCAA A
10   20   30   40   50   60   70   80   90   100   110   120   130   140

GCCCCCAGCA CTCCTG TGCCACC CAGCCCAG CCCCTGG ACTCACCAAG CGTG TG AAN AAAANT AAACAGCCACT TCAGG TG ACCAAGG ATCTGGG CCGCTGA A AGCCTGCAAATG ACCTCCTGCT CATA AATGCTG
150   160   170   180   190   200   210   220   230   240   250   260   270   280

TGT TGCANACCAACG ACCTGACCTCCG TCCACCTGGG CGTNAAATTCAGCTGCCGCTTCACCCT TCGGG AGGTCCAGGAGCG T TGG TACGCCCTGCTCTACNATCCTGTCATCTCCAAGTTGG CCTGTCAGG CCATGAGNG
290   300   310   320   330   340   350   360   370   380   390   400   410   420

CAGCTGCACCCAGAGNG CTATTGCAGCATCCAAA NCA AGGCCCTGT TAGCA AGG CTGANG AACANCTGCTGANCACCTTCCAGGAACTGCTGCACAN ACACCC
430   440   450   460   470   480   490   500   510   520   530   540   550   560

TGA TGCCTTCTACCTGGCCCGTACCG CG AAA GGCCTGCANGCCCACTGGCA CTCATGAACANTNTT ACCTG NTGG AAGANCAAAAANTTGCA NCCNCTNCCCNA ANGGGA C AANTT CTNAACTTCTCT
570   580   590   600   610   620   630   640   650   660   670   680

mbp3nt [1 to 1257] -> 1-phase Translation

DNA sequence   1603 b.p.   GTGGATCCCCCG ... TCGCCCTATAGT   linear
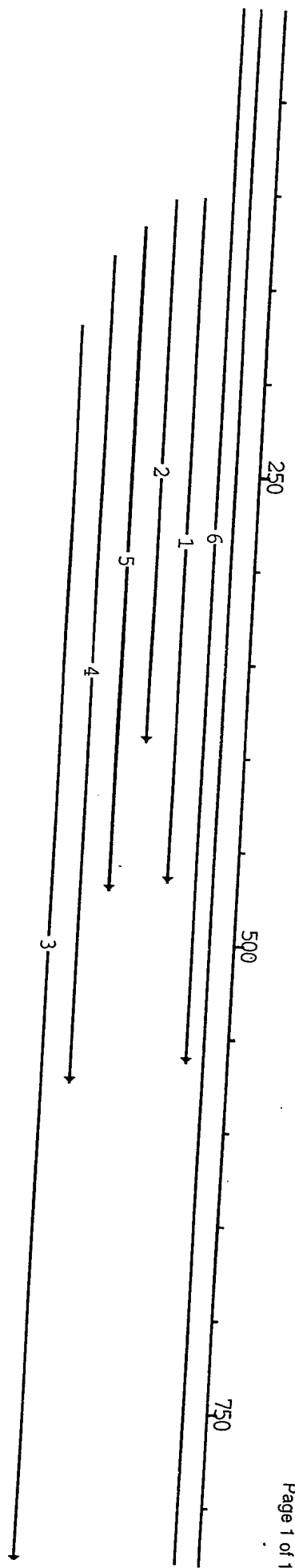
4909+8855+8955+8856+6196 mekk1bp3

```
1/1                              31/11
GTG GAT CCC CCG GGC TGC AGG AAT TCG GCA CGA GGT GGG GTG GAA CCA GGG CGC TGT TCG
 V   D   P   P   G   C   R   N   S   A   R   G   G   V   E   P   G   R   C   S
61/21                            91/31
GGG AGT GAA CCC TCC TCC AGT GAG AAA AAG AAG GTA TCC AAA GCC CCC AGC ACT CCT GTG
 G   S   E   P   S   S   S   E   K   K   K   V   S   K   A   P   S   T   P   V
121/41                           151/51
CCA CCC AGC CCA GCC CCA GCC CCT GGA CTC ACC AAG CGT GTG AAg AAg AGT AAA CAG CCA
 P   P   S   P   A   P   A   P   G   L   T   K   R   V   K   K   S   K   Q   P
181/61                           211/71
CTT CAG GTG ACC AAG GAT CTG GGC CGC TGG AAg CCT GCA AAT GAC CTC CTG CTC ATA AAT
 L   Q   V   T   K   D   L   G   R   W   K   P   A   N   D   L   L   L   I   N
241/81                           271/91
GCT GTG TTG CAg ACC AAC GAC CTG ACC TCC GTC CAC CTG GGC GTG AAA TTC AGC TGC CGC
 A   V   L   Q   T   N   D   L   T   S   V   H   L   G   V   K   F   S   C   R
301/101                          331/111
TTC ACC CTT CGG GAG GTC CAG GAG CGT TGG TAC GCC CTG CTC TAC gAT CCT GTC ATC TCC
 F   T   L   R   E   V   Q   E   R   W   Y   A   L   L   Y   D   P   V   I   S
361/121                          391/131
AAG TTG GCC TGT CAG GCC ATG AGG CAG CTG CAC CCA GAG GCT ATT GCA GCC ATC CAG AGC
 K   L   A   C   Q   A   M   R   Q   L   H   P   E   A   I   A   A   I   Q   S
421/141                          451/151
AAG GCC CTG TTT AGC AAG GCT GAG GAG CAG CTG CTG AGC AAA GTG GGA TCG ACC AGC CAG
 K   A   L   F   S   K   A   E   E   Q   L   L   S   K   V   G   S   T   S   Q
481/161                          511/171
CCC ACC TTG GAG ACC TTC CAG GAC CTG CTG CAC AGA CAC CCT GAT GCC TTC TAC CTG GCC
 P   T   L   E   T   F   Q   D   L   L   H   R   H   P   D   A   F   Y   L   A
541/181                          571/191
CGT ACC GCG AAG GCC CTG CAG GCC CAC TGG CAG CTC ATG AAG CAG TAT TAC CTG CTG GAG
 R   T   A   K   A   L   Q   A   H   W   Q   L   M   K   Q   Y   Y   L   L   E
601/201                          631/211
GAC CAG ACA GTG CAG CCG CTG CCC AAA GGG GAC CAA GTG CTG AAC TTC TCT GAT GCA GAG
 D   Q   T   V   Q   P   L   P   K   G   D   Q   V   L   N   F   S   D   A   E
661/221                          691/231
GAC CTG ATT GAT GAC AGT AAG CTC AAG GAC ATG CGA GAT GAG GTC CTG GAA CAT GAG CTG
 D   L   I   D   D   S   K   L   K   D   M   R   D   E   V   L   E   H   E   L
721/241                          751/251
ATG GTG GCT GAC CGG CGC CAG AAG CGA GAG ATT CGG CAG CTG GAA CAG GAA CTG CAT AAG
 M   V   A   D   R   R   Q   K   R   E   I   R   Q   L   E   Q   E   L   H   K
781/261                          811/271
TGG CAG GTG CTA GTG GAC AGC ATC ACA GGC ATG AGC TCT CCG GAC TTC GAC AAC CAg ACA
 W   Q   V   L   V   D   S   I   T   G   M   S   S   P   D   F   D   N   Q   T
841/281                          871/291
CTG GCA GTG CTG CGG GGC CGC ATG GTG CGG TAC CTG ATG CGC TCG CGT GAG ATC ACC CTG
 L   A   V   L   R   G   R   M   V   R   Y   L   M   R   S   R   E   I   T   L
901/301                          931/311
GGC AGA GCA ACC AAG GAT AAC CAG ATT GAT GTG GAC CTG TCT CTG GAG GGT CCG GCC TGG
 G   R   A   T   K   D   N   Q   I   D   V   D   L   S   L   E   G   P   A   W
961/321                          991/331
AAG ATA TCC CGG AAA CAA GGT GTC ATC AAG CTG AAG AAC AAC GGT GAT TTC TTC ATT GCC
 K   I   S   R   K   Q   G   V   I   K   L   K   N   N   G   D   F   F   I   A
1021/341                         1051/351
AAT GAG GGT CGA CGG CCC ATC TAC ATC GAT GGA CGG CCG GTG CTC TGT GGC TCC AAA TGG
 N   E   G   R   R   P   I   Y   I   D   G   R   P   V   L   C   G   S   K   W
1081/361                         1111/371
CGC CTC AGC AAC AAC TCT GTG GTG GAG ATC GCC AGC CTG CGA TTC GTC TTC CTT ATC AAC
 R   L   S   N   N   S   V   V   E   I   A   S   L   R   F   V   F   L   I   N
1141/381                         1171/391
CAG GAC CTC ATT GCC CTC ATC AGG GCT GAG CTG CCA AGA TCA CAC CAC AGT GAG GAA TGG
 Q   D   L   I   A   L   I   R   A   E   L   P   R   S   H   H   S   E   E   W
1201/401                         1231/411
TGG CAG GAC TCG TGG GCC CTC TCC GGC CTG TTT CCC CTG CCA CTC CAG CCC CCT TGA
 W   Q   D   S   W   A   L   S   G   L   F   P   L   P   L   Q   P   P   *
```

Applied Biosystems

AutoAssembler™ 1.4.0

Ass EST

250

500

750

2

1

6

5

4

3

Project: **Ass EST**
Last saved: ▓▓▓▓▓▓▓▓▓▓▓▓▓   16:09:01
Last assembled: ▓▓▓▓▓▓▓▓▓▓▓▓▓   16:09:55

Threshold: 10.0 Error Rate: 5.0%
Window: 13 Offset: 0 Tolerance: 1 Hit Count: 10 Overlap: 10%

	Sequences	Bases	Percent
Total in project:	6	2576	100.0%
Total in assemblages:	6	2576	100.0%
Total unassembled:	0	0	0.0%
Total dye primer:	0	0	0.0%
Total dye terminator:	0	0	0.0%
Non-373 sequences:	6	2666	103.5%

	Sequences	Bases	Score	Ambiguities
w26888.Assemblage.1	6	831	1773.0	34

---

w26888.Assemblage.1   Sequences: 6 Bases: 831 Score: 1773.0
   Redundancy   Average: 3.2 High: 6 Low: 1
   Sequence Lengths   Average: 429 High: 640 Low: 282

File	Sample		ID	Begin	End	Length	Date	Chemistry
w26888		->	6	0	562	535	12/03/97	
aa134651		->	1	103	467	352	12/03/97	
f12127		->	2	104	392	282	12/03/97	
w00383		->	5	119	472	347	12/03/97	
t66207		->	4	135	575	420	12/03/97	
r52839		->	3	172	831	640	12/03/97	

Unassembled Sequences   Sequences: 0 Bases: 0
File	Sample	ID	Begin	End	Length	Date	Chemistry

SIMBPS XS

© Applied Biosystems

AutoAssembler™ 1.4.0

untitled 2

```
                                25              50              75              100
w26888.Assemblage.1  GGnnnnTACCCAGGACGCGACCCTCCAGAGACAGAGGTCCACATCAATCTGGTTATCCTTGGTTGCTCTGCCCAGGTGATCTCACGCGGAGCGCATCAGTCAGTACCGCGAGAGAAGCcggCTTT-G|
                                                                                                                                      · · ·
w26888           ->                                  GGnnnnTACCCAGGACGCGACCCTCCAGAGACAGAGGTCCACATCAATCTGGTTATCCTTGGTTGCTCTGCCCAGGTGATCTCACGCGGAGCGCATCAGTACCGCGAGAGAAGCCggCTTT-G
aa134651         ->                                                                                                                 ACGGAAGCCGGCTTT-G
f12127           ->                                                                                                                 CGGAAGCGNNCTTTTG
w00383           ->                                                                                                                 G
```

```
                                125             150             175             200             225
w26888.Assemblage.1  GCCCTGCGGCTGCTACCGTCGCCGCGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
                                                                      ·
w26888           ->  GCCCTGCGGGCTGCTACCGTCGCCGCGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGNT
aa134651         ->  GCC--TGCGGCTGCTACCGTCGCCGCGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
f12127           ->  GCCCTGCGGGCTGCTACCGTCGCNCGNGGAGAAATTGTTGGNTCTGGCAGTCTAGGAATGAATCTCTCTCAGCNTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
w00383           ->  GCC--TGCGGCTGCTACCGTCGCCGCGGAGAAATTGTTGGANCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
t66207           ->          CCGTCGCC--CGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
r52839           ->          CCGTCGCC--CGGAGAAATTGTTGGATCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
```

```
                                250             275             300             325             350
w26888.Assemblage.1  CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGACTGGTAAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGCATCAGGCACT-GCCAGCCG-CTCA-GAG
                                ·
w26888           ->  CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGACTGGTAAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGNATCAGGCACT-GCCAGNCG-CTCAAGAG
aa134651         ->  CCTCCTAGCCCGTGGTTTGGAACCAGTGGCTTTGGGACTGGTAAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGCATCAGGCACT-GCCAGCCG-CTCA-GAG
f12127           ->  CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGACTGGTAAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGCATCAGGCACT-GCCAGCCNGCTCA-GAG
w00383           ->  CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGACTGGTNAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGCATCAGGCACTTGCAGCCCG-CTCA-GAG
t66207           ->  CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGACTGGTAAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGCATCAGGCACT-GC-AGCCG-CTCA-GAG
r52839           ->  CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGGACTGGTAAGAGGATGGACAAAGATTCTCAGGGGCTGTAGATTCATCCCTGATGGCATCAGGCACT-GCCAGCCG-CTCA-GAG
```

```
                                375             400             425             450             475
w26888.Assemblage.1  GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGG-a-CCATCCC-TAAAC-GGAGAA-GCTCCTCCAaGgT-CATCAAGAGGAAGAAGTtC-GaTGAT
                                ·                    · · ·                          ·
w26888           ->  GATGAGGAGTCACTGGCAGGGNA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGG-a-CCATCCC-TAAAC-GGAGAA-GNTCCTCCAGGT-CANCAAGAGGA-GAAGT-CCGNTGAT
aa134651         ->  GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCGA-GCCTCC-TCCCAAGGCCTTGGG-NACCATCCC-TAAAC-GGAGAA-GCTCCTCCAAGGTTCATCAAGAGGAAG
f12127           ->  GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCAAGGCCTTGGG-CACCATCCC-TAAAC-GGAGAA-GCTCCTCCAAGGTTCATCAAGAGGAAG
w00383           ->  GATGAGGAGTCACTGGCAGGGCA-GAA-GN-G
t66207           ->  GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCAAGGCCTTNGG-A-CCAATCCCGGAGAAAGC-GAAGCCTCC-TCCCAAGGTTCATCAAGAGGAAGNAGTT
r52839           ->  GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGG-A-CCAATCCC-TAAAC-GGAGAA-GCTCCTCCAAGGTT-TATCAAGAGGAAGAAGTTC-GATGAT
```

Applied
Biosystems

untitled 2

AutoAssembler™ 1.4.0

```
                    500            525            550            575            600
w26888.Assemblage.1 GAgcTtgGtGGAGAgcAGCCTGGmAAaaTcTtcTtaCCCggCggCAAAGGGGgCCAgt~GGG~tkGAacCAGGGGgcgcTtktT~CGGGGAGTGAACCcTTCCTCCcAGTGAGAAGAGAGAAGGTATT
w26888          ->  GAATTTNGNGGAGAAAAGCCTGGAAA--TNT-CTT-CCCCGN-AAAGGGG-CAAN--GGG-NTGACCCAGGGG---TTNT-CG

t66207          ->  GAGCTtGGTtGGAGAGcAGCagCCTtGGNAAAaTCTtCTtaCCCGGGCAAAGGGGGCCAGTtGGG-TNGAACCAGGGGGCGCTNTtTTCGGGGAGTGAACC--T
r52839          ->  GAGCTtGGTtGGAGAGcAGCagCagCCTtGGCAAAaTCTtCT-ACCCGGGCAAAGGGGGGCCAGT-CGGGTGGAACCAGGG-CGCTGTT-CGGGGAGTGAACCCcTTCCTCCcAGTGAGAAGAGAGAAGGTATT

                    625            650            675            700
w26888.Assemblage.1 CCAAAGCCCCCCAGCACTCCTGTGCCCACCCAGCCCCCAGCCCCCAGCCCCCTGGGATTCACCCAAGCGTGTGAAGAAGAGTAAACAGCCATTTTCAGTGAACCAAGGATCTTGGGCGCGTTGGAA

r52839          ->  CCAAAGCCCCCCAGCACTCCTGTGCCCACCCAGCCCCCAGCCCCCTGGGATTCACCCAAGCCCCCGGGATTCACCCAAGCGTGTGAAGAAGAGTAAACAGCCATTTTCAGTGAACCAAGGATCTTGGGCGCGTTGGAA

                    725            750            775            800            825
w26888.Assemblage.1 GCTTGCAGATTGAnCTTCTTnTTATTAAATTGTTGTGTTTGCAGAGACCAACGACTTAACTTCnTTCACTTGGGnTGAAATTnAGTTnCCGTTTAACCTTTnGGAAGTTCAG

r52839          ->  GCTTGCAGATTGANCTTCTTnTTATTAAATTGTTGTGTTTGCAGAGACCAACGACTTAACTTCnTTCACTTGGGnTGAAATTTnAGTTnCCGTTTAACCTTTnGGAAGTTCAG
```

ABI PRISM™

Model 377
Version 3.0
ABI100
Version 3.0

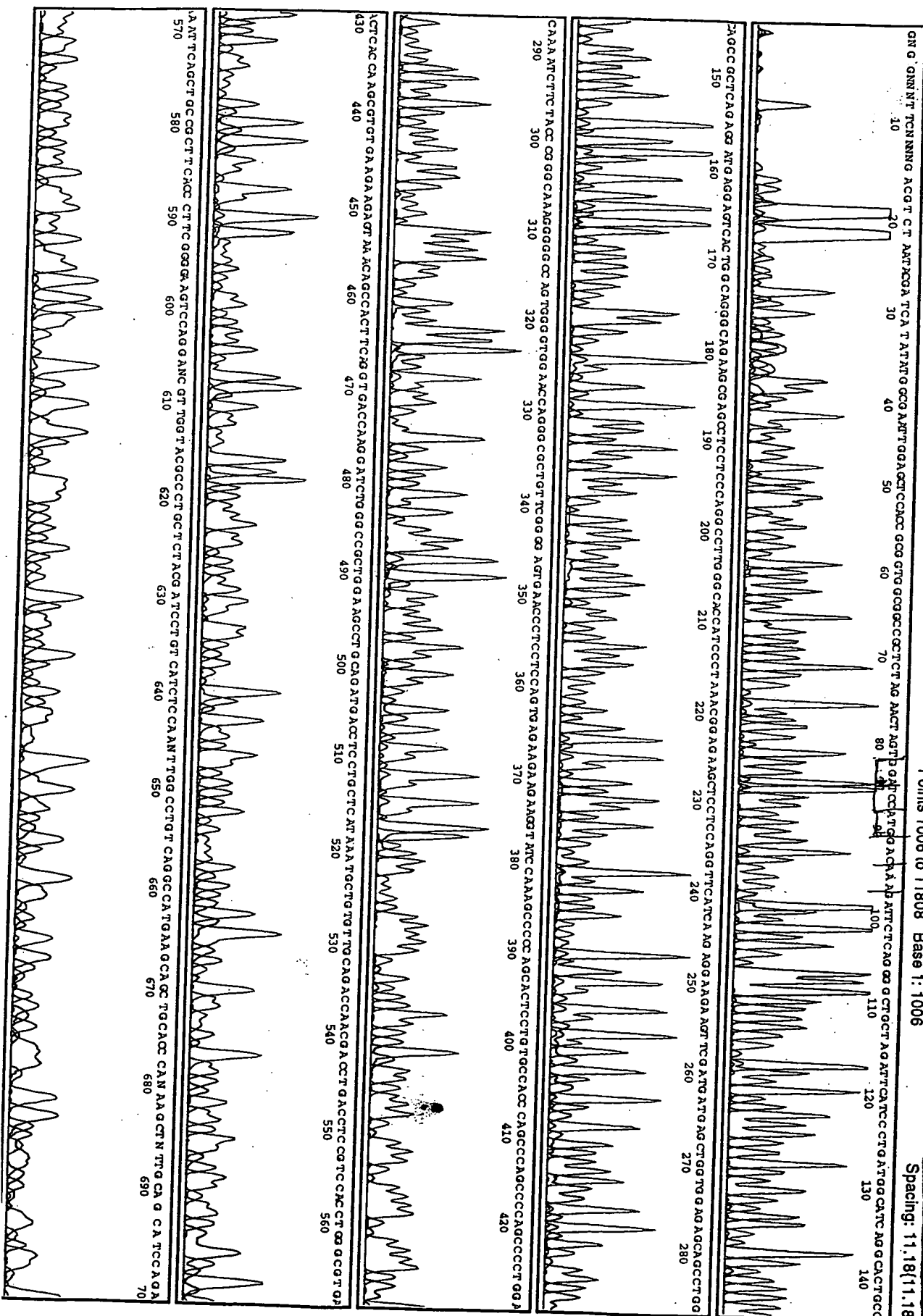09•CM 13

CM 13
Lane 9

Signal G:104 A:318 T:111 C:113
DT4%Ac{A Set-AnyPrimer)
SN 9508O645
Points 1006 to 11808   Base 1: 1006

Spacing: 11.18(11.18)
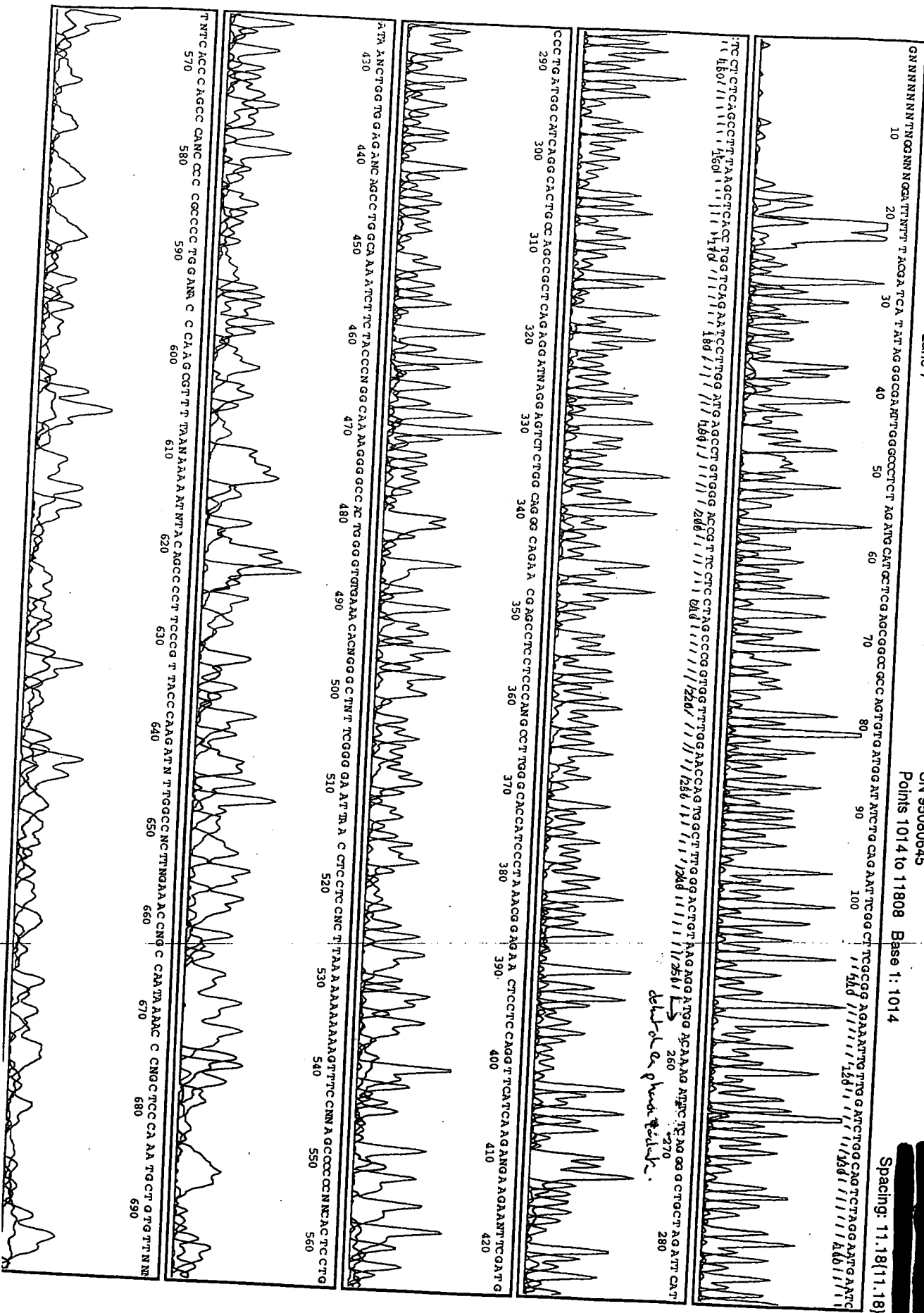
ABI
PRISM™
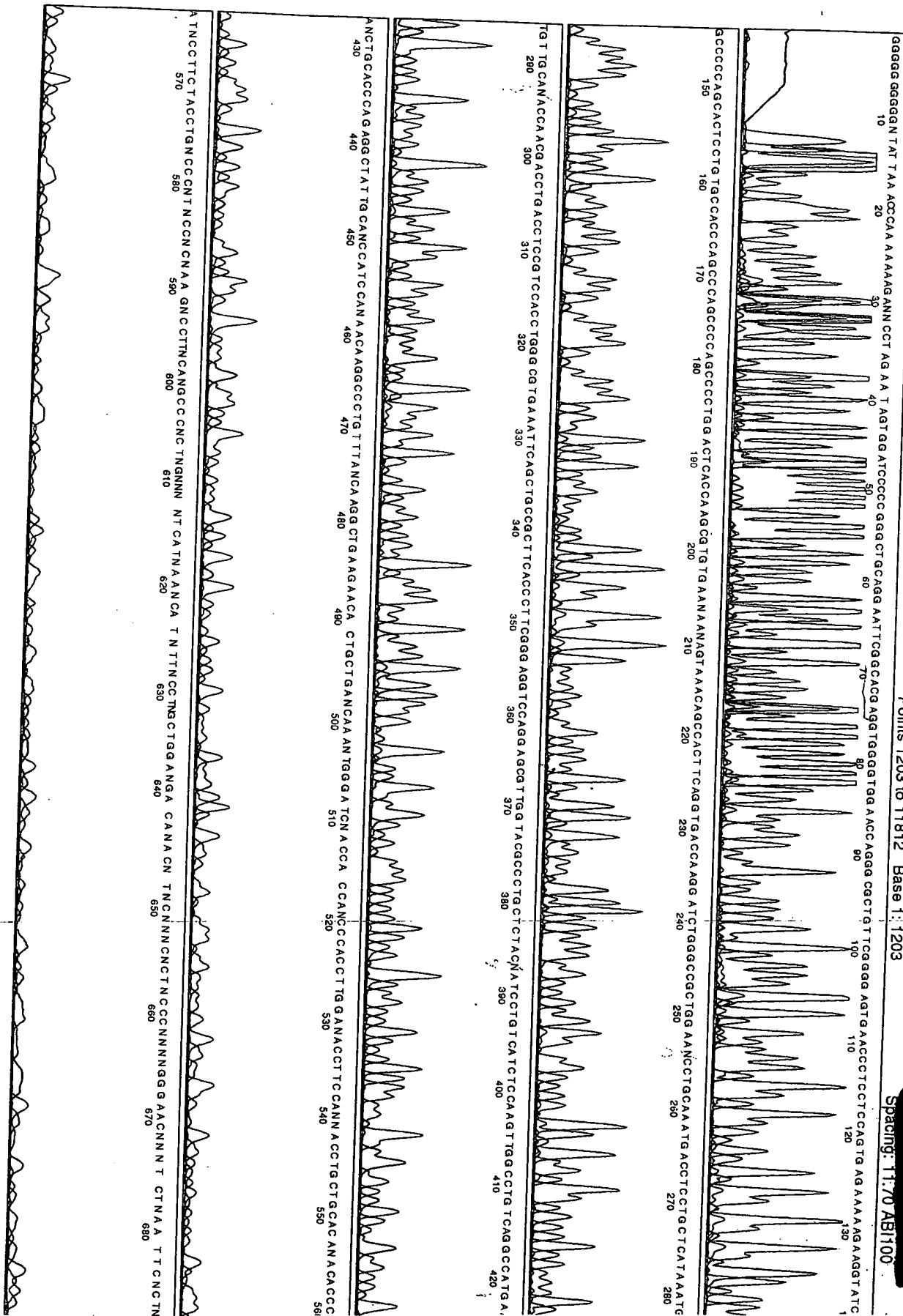
Model 377
Version 3.0
ABI100
Version 3.0

07•CM 21

CM 21
Lane 7

Signal G:104 A:448 T:303 C:232
DT4%Ac(A Set-AnyPrimer)
SN 9508645
Points 1014 to 11808   Base 1: 1014

Spacing: 11.18(11.18)

Page 1 of 2

GGGGG GGGGGN TAT TAA ACCCAA A A AAAAGANN CCT AG A A T AGTGG ATCCCCC GGGGCT GCAGG AATTCGG CACG AGGTGGGGGTGG AACCAGGG CGCTGTTCGGGG AGTGAACCCTCCTCCAGTG AG AAAAAGA AAGGT ATC
10   20   30   40   50   60   70   80   90   100   110   120   130

GCCCCCAGCACTCCTG TGCCACCCCAGCCCCCAGCCCCCTGG ACTCACCA AGCG TG TG AANA ANAGTAAACAGCCACT TCAGG TGACCCA AGG ATCTGGGCGCGCTGG AANCCTGCAAATGACCTCCTGCTCATAAATG
150   160   170   180   190   200   210   220   230   240   250   260   270   280

TG T TGCANACCA ACG ACCTGACCTCCG TCCACCTGGG CG TGAAATTCAGCTGCCGCTTCACCCTTCGGG AGGTCCAGGAGCGTTGG ATACGCCCCTGCTCTACNATCCTGTCATCTCCAAGTGGCCTG TCAGGCCATGA
280   300   310   320   330   340   350   360   370   380   390   400   410   420

ANCTGCACCCAG AGG CTATTG CANCCATCCANACA AGGCCCTG TTANCAAGG CTGAAGAACA CTGCTGANCAA AN TGGG A TCN A CCA CCANCCCACCTTG GANACCTTCCANN ACCTGCTGCAC ANACACCC
430   440   450   460   470   480   490   500   510   520   530   540   550   56(

A TNCCTTCTACCTGNCCCNTNCCNCNCNAA GNCCTTNCANGCC CNC TNGNNN NT CATNAANCA T N TTNCC TNGCTGG ANGA CANA CN TNCNNNCNCTNCCCNNNNGG G AACNNNN T CTNAA T TCNCTN
570   580   590   600   610   620   630   640   650   660   670   680

ABI PRISM

Model 377
Version 2.1.1

20•CM 3

CM 3
Lane 20

Signal G:483 A:1087 T:367 C:416
*DT4%(Ac(A Set-AnyPrimer)
S/N 9508645
Points 1209 to 11812   Base 1:1209

Spacing: 11.29 ABI700